FIGURE 1
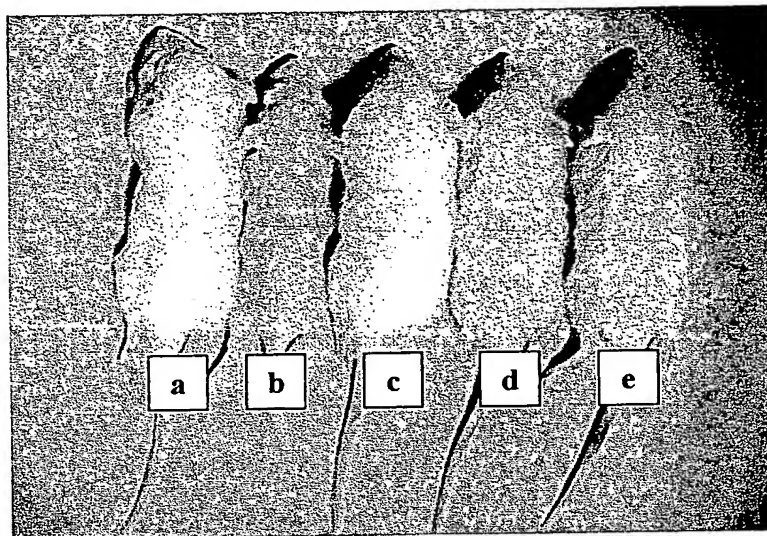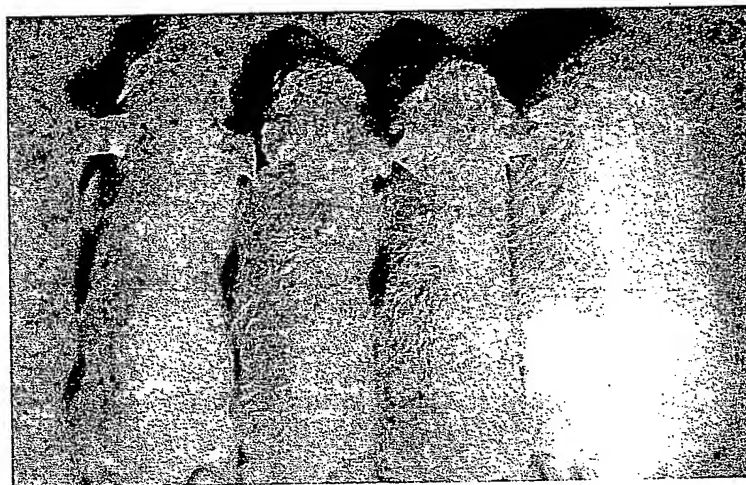

a   untreated control

b   Ara-c control

c   SEQ ID NO: 2

d   SEQ ID NO: 3

e   SEQ ID NO: 22

FIGURE 2

Ara-c control   *Ara-c* +SEQ ID NO: 10
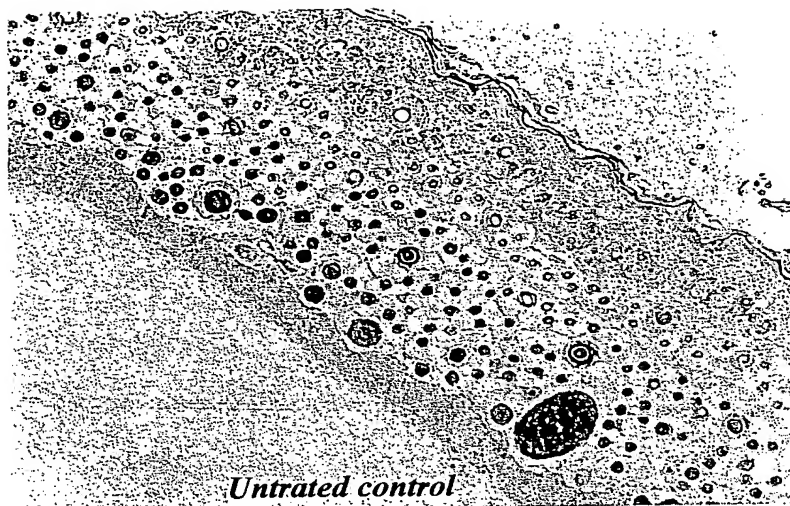
0.1mg   *0.5mg*   *2.5mg*

FIGURE 3A

Untrated control

FIGURE 3B

Ara-c control

FIGURE 3C

Ara-c + SEQ ID NO: 21

FIGURE 4

HFL-1 cell proliferation in the presence of TGF-beta peptides
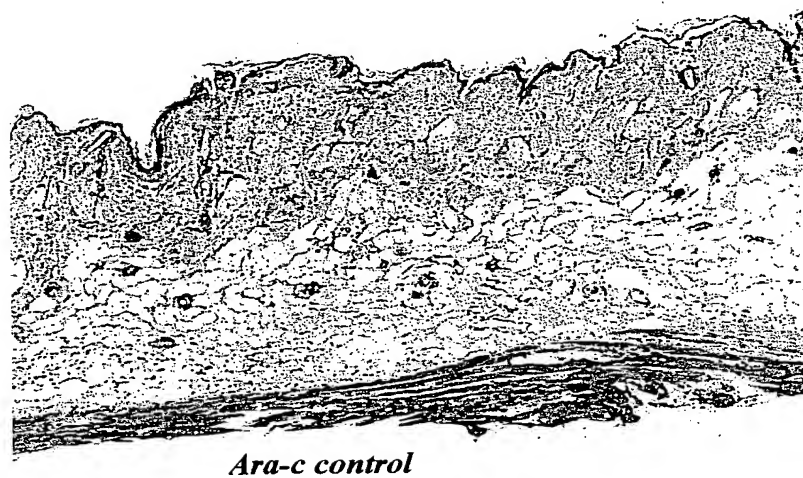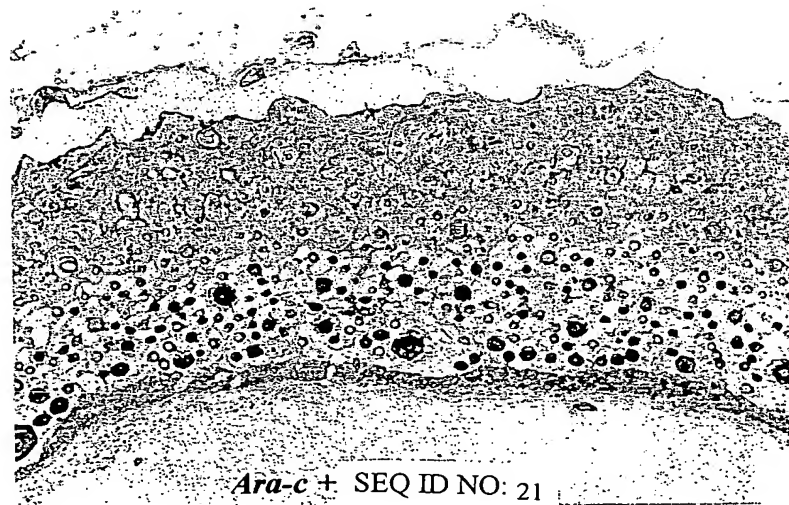
O: SEQ ID NO: 22
● SEQ ID NO: 21
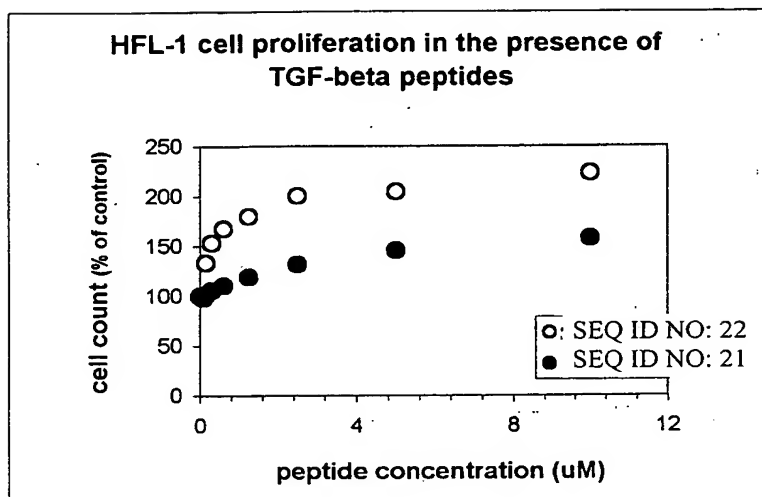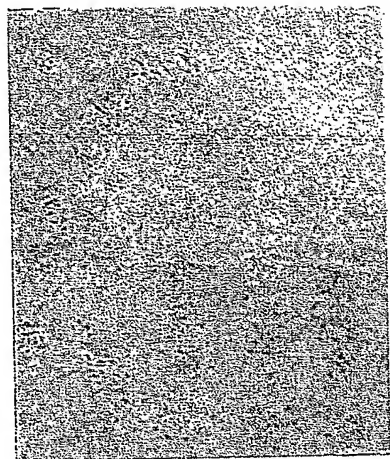
FIGURE 5A

FIGURE 5B
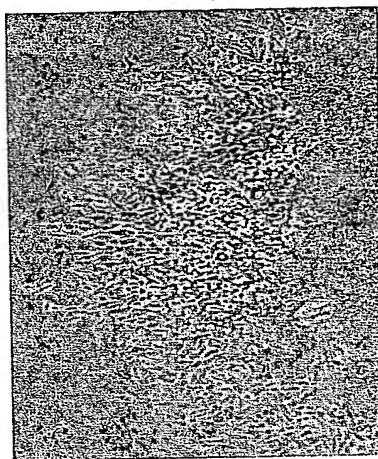
FIGURE 5C
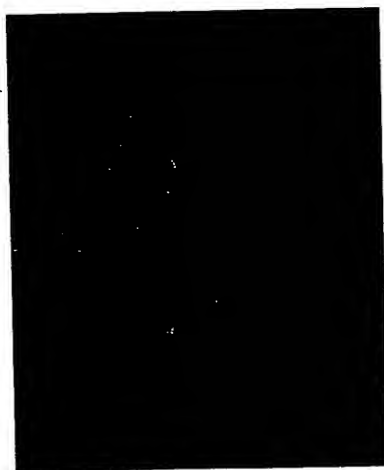
FIGURE 5D
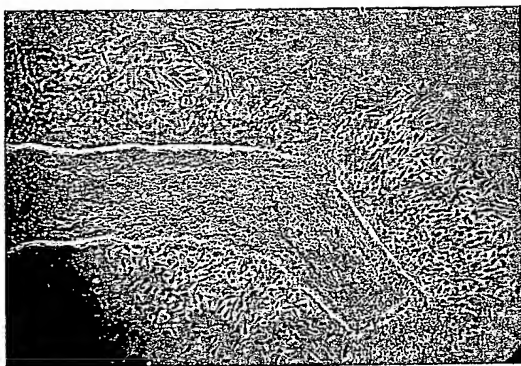
FIGURE 6A

FIGURE 6B
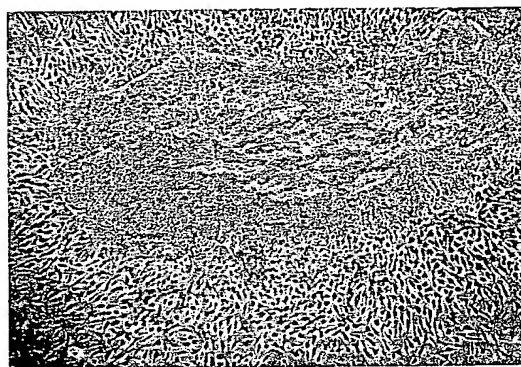
FIGURE 6C
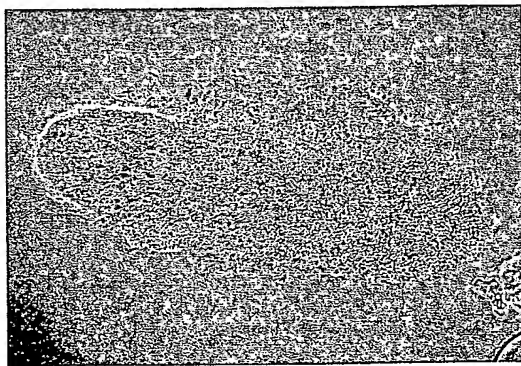
FIGURE 6D
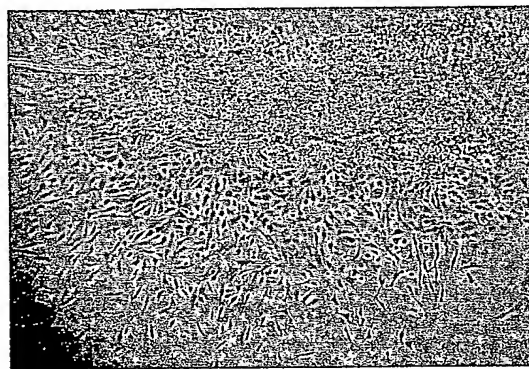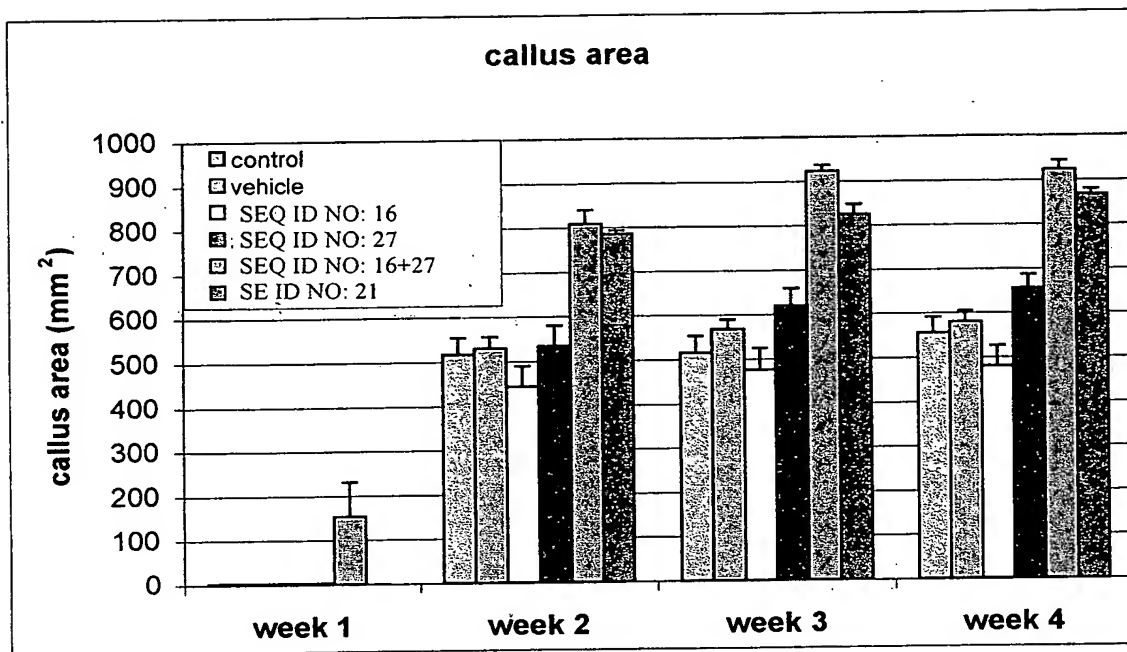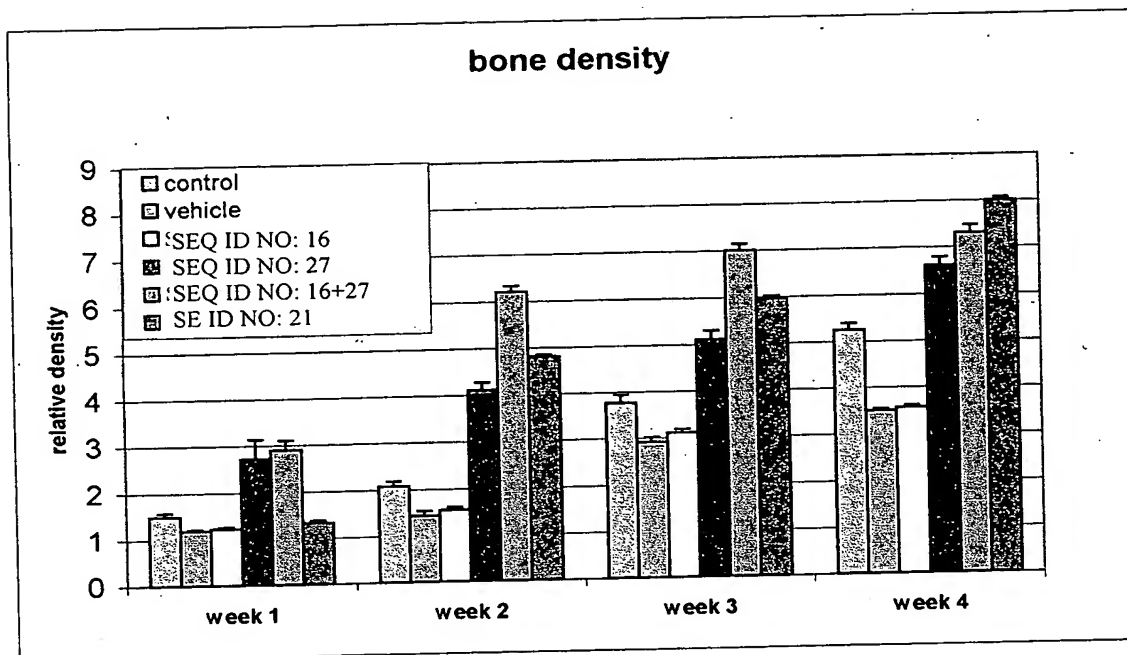
FIGURE 7

callus area

FIGURE 8

bone density

Legend:
- □ control
- ▣ vehicle
- □ SEQ ID NO: 16
- ▦ SEQ ID NO: 27
- ▣ SEQ ID NO: 16+27
- ▦ SE ID NO: 21

relative density (y-axis: 0–9)

week 1   week 2   week 3   week 4

FIGURE 9

bone healing grading
(scale 1 to 10 as judged by x-ray examination)

Legend:
- control
- vehicle
- SEQ ID NO: 16
- SEQ ID NO: 27
- SEQ ID NO: 16+27
- SE ID NO: 21
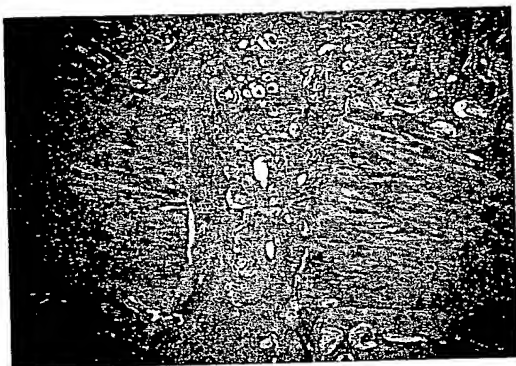
FIGURE 10A   FIGURE 10B

FIGURE 11A

FIGURE 11B
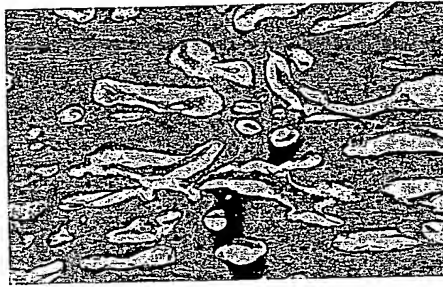
Fig 12

HJ-loop

```
TBR1        EIARRCSIGGI---HEDYQLPYYDLVPSDPSVEE
ACTR2       ELVSRCKAADG--PVDEYMLPFEEEIGQHPSLEE
BMR2        EIFMRCTDLFPGESVPEYQMAFQTEVGNHPTFED
TBR2        EMTSRCNAVGE---VKDYEPPFGSKVREHPCVES
ALK4        EIARRCNSGGV---HEEYQLPYYDLVPSDPSIEE
ALK3        EMARRCITGGI---VEEYQLPYYNMVPSDPSYED
ALK1        EIARRTIVNGI---VEDYRPPFYDVVPNDPSFED
            *:   *          :*  .:   :  ..*   *.
```

Alpha-D region
CLUSTAL X (1.81) multiple sequence alignment

```
TBR1        ----SDYHEHGSLFDYLNRYTVTVE
ACTR2       ----TAFHDKGSLTDYLKGNIITWNE
BMR2        ----MEYYPNGSLCKYLSLHTSDWV
TBR2            TAFHAKGNLQEYLTRHVISWE
ALK4        ----SDYHEHGSLFDYLNRYTVTIE
ALK3        ----TDYHENGSLYDFLKCATLDTR
ALK1        ----THYHEHGSLYDFLQRQTLEPH
                ::  :*.*  .:*
```

B4-B5 region

```
TBR1        ADNKDNG-TWTQLWLVSD
ACTR2       AEKRGSS-LEAELWLITA
BMR2        GDERVTADGRMEYLLVME
TBR2        AEERKTE-LGKQYWLITA
ALK4        ADNKDNG-TWTQLWLVSD
ALK3        ADIKGTG-SWTQLYLITD
ALK1        SDMTSRN-SSTQLWLITH
            .:          :   *:
```

A-region

```
TBR1        ----QTVMLRHENILGFIA
ACTR2       ----STPGMKHENLLQFIA
BMR2        ----RVPLMEHDNIARFIV
TBR2            SDINLKHENILQFLT
ALK4        ----QTVMLRHENILGFIA
ALK3        ----QTVLMRHENILGFIA
ALK1        ----NTVLLRHDNILGFIA
                :.*:*:   *:.
```